

Input Set: I155252.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

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1  <110> APPLICANT: Evans, Ronald M.
2      Forman, Barry M.
3  <120> TITLE OF INVENTION: SELECTIVE MODULATORS OF PEROXISOME
4      PROLIFERATOR ACTIVATED RECEPTOR-GAMMA, AND METHODS FOR THE
5      USE THEREOF
6  <130> FILE REFERENCE: SALK1470-2
7  <140> CURRENT APPLICATION NUMBER: US/09/155,252
8  <141> CURRENT FILING DATE: 1998-09-21
9  <150> EARLIER APPLICATION NUMBER: PCT/US96/05465
10 <151> EARLIER FILING DATE: 1996-04-18
11 <160> NUMBER OF SEQ ID NOS: 7
12 <170> SOFTWARE: FastSEQ for Windows Version 4.0
13 <210> SEQ ID NO 1
14 <211> LENGTH: 2005
15 <212> TYPE: DNA
16 <213> ORGANISM: Mus musculus
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18 <221> NAME/KEY: CDS
19 <222> LOCATION: (352)...(1776)
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23      gggaccgagt gtgacgacaa ggtgaccggg ctgaggggac gggctgagga gaagtcacac      180
24      tctgacagga gcctgtgaga ccaacagcct gacggggtct cggttgaggg gacgcgggct      240
25      gagaagtcac gttctgacag gactgtgtga cagacaagat ttgaaagaag cggtgaacca      300
26      ctgatattca ggacattttt aaaaacaaga ctacccttta ctgaaattac c atg gtt      357
27                                     Met Val
28                                     1
29      gac aca gag atg cca ttc tgg ccc acc aac ttc gga atc agc tct gtg      405
30      Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val
31          5              10              15
32      gac ctc tcc gtg atg gaa gac cac tcg cat tcc ttt gac atc aag ccc      453
33      Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro
34          20              25              30
35      ttt acc aca gtt gat ttc tcc agc att tct gct cca cac tat gaa gac      501
36      Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Ala Pro His Tyr Glu Asp
37          35              40              45              50
38      att cca ttc aca aga gct gac cca atg gtt gct gat tac aaa tat gac      549
39      Ile Pro Phe Thr Arg Ala Asp Pro Met Val Ala Asp Tyr Lys Tyr Asp
40          55              60              65
41      ctg aag ctc caa gaa tac caa agt gcg atc aaa gta gaa cct gca tct      597
42      Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser
43          70              75              80
44      cca cct tat tat tct gaa aag acc cag ctc tac aac agg cct cat gaa      645

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45	Pro	Pro	Tyr	Tyr	Ser	Glu	Lys	Thr	Gln	Leu	Tyr	Asn	Arg	Pro	His	Glu	
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47	gaa	cct	tct	aac	tcc	ctc	atg	gcc	att	gag	tgc	cga	gtc	tgt	ggg	gat	693
48	Glu	Pro	Ser	Asn	Ser	Leu	Met	Ala	Ile	Glu	Cys	Arg	Val	Cys	Gly	Asp	
49		100					105					110					
50	aaa	gca	tca	ggc	ttc	cac	tat	gga	gtt	cat	gct	tgt	gaa	gga	tgc	aag	741
51	Lys	Ala	Ser	Gly	Phe	His	Tyr	Gly	Val	His	Ala	Cys	Glu	Gly	Cys	Lys	
52		115				120					125					130	
53	ggg	ttt	ttc	cga	aga	acc	atc	cga	ttg	aag	ctt	att	tat	gat	agg	tgt	789
54	Gly	Phe	Phe	Arg	Arg	Thr	Ile	Arg	Leu	Lys	Leu	Ile	Tyr	Asp	Arg	Cys	
55				135					140					145			
56	gat	ctt	aac	tgc	cgg	atc	cac	aaa	aaa	agt	aga	aat	aaa	tgt	cag	tac	837
57	Asp	Leu	Asn	Cys	Arg	Ile	His	Lys	Lys	Ser	Arg	Asn	Lys	Cys	Gln	Tyr	
58			150						155				160				
59	tgt	cgg	ttt	cag	aag	tgc	ctt	gct	gtg	ggg	atg	tct	cac	aat	gcc	atc	885
60	Cys	Arg	Phe	Gln	Lys	Cys	Leu	Ala	Val	Gly	Met	Ser	His	Asn	Ala	Ile	
61		165					170					175					
62	agg	ttt	ggg	cgg	atg	cca	cag	gcc	gag	aag	gag	aag	ctg	ttg	gcg	gag	933
63	Arg	Phe	Gly	Arg	Met	Pro	Gln	Ala	Glu	Lys	Glu	Lys	Leu	Leu	Ala	Glu	
64		180					185				190						
65	atc	tcc	agt	gat	atc	gac	cag	ctg	aac	cca	gag	tct	gct	gat	ctg	cga	981
66	Ile	Ser	Ser	Asp	Ile	Asp	Gln	Leu	Asn	Pro	Glu	Ser	Ala	Asp	Leu	Arg	
67		195			200					205					210		
68	gcc	ctg	gca	aag	cat	ttg	tat	gac	tca	tac	ata	aag	tcc	ttc	ccg	ctg	1029
69	Ala	Leu	Ala	Lys	His	Leu	Tyr	Asp	Ser	Tyr	Ile	Lys	Ser	Phe	Pro	Leu	
70				215					220					225			
71	acc	aaa	gcc	aag	gcg	agg	gcg	atc	ttg	aca	gga	aag	aca	acg	gac	aaa	1077
72	Thr	Lys	Ala	Lys	Ala	Arg	Ala	Ile	Leu	Thr	Gly	Lys	Thr	Thr	Asp	Lys	
73			230					235					240				
74	tca	cca	ttt	gtc	atc	tac	gac	atg	aat	tcc	tta	atg	atg	gga	gaa	gat	1125
75	Ser	Pro	Phe	Val	Ile	Tyr	Asp	Met	Asn	Ser	Leu	Met	Met	Gly	Glu	Asp	
76		245					250				255						
77	aaa	atc	aag	ttc	aaa	cat	atc	acc	ccc	ctg	cag	gag	cag	agc	aaa	gag	1173
78	Lys	Ile	Lys	Phe	Lys	His	Ile	Thr	Pro	Leu	Gln	Glu	Gln	Ser	Lys	Glu	
79		260				265				270							
80	gtg	gcc	atc	cga	att	ttt	caa	ggg	tgc	cag	ttt	cga	tcc	gta	gaa	gcc	1221
81	Val	Ala	Ile	Arg	Ile	Phe	Gln	Gly	Cys	Gln	Phe	Arg	Ser	Val	Glu	Ala	
82		275			280				285					290			
83	gtg	caa	gag	atc	aca	gag	tat	gcc	aaa	aat	atc	cct	ggg	ttc	att	aac	1269
84	Val	Gln	Glu	Ile	Thr	Glu	Tyr	Ala	Lys	Asn	Ile	Pro	Gly	Phe	Ile	Asn	
85			295					300					305				
86	ctt	gat	ttg	aat	gac	caa	gtg	act	ctg	ctc	aag	tat	ggg	gtc	cat	gag	1317
87	Leu	Asp	Leu	Asn	Asp	Gln	Val	Thr	Leu	Leu	Lys	Tyr	Gly	Val	His	Glu	
88			310					315					320				
89	atc	atc	tac	acg	atg	ctg	gcc	tcc	ctg	atg	aat	aaa	gat	gga	gtc	ctc	1365
90	Ile	Ile	Tyr	Thr	Met	Leu	Ala	Ser	Leu	Met	Asn	Lys	Asp	Gly	Val	Leu	
91		325					330					335					
92	atc	tca	gag	ggc	caa	gga	ttc	atg	acc	agg	gag	ttc	ctc	aaa	agc	ctg	1413
93	Ile	Ser	Glu	Gly	Gln	Gly	Phe	Met	Thr	Arg	Glu	Phe	Leu	Lys	Ser	Leu	
94		340					345					350					

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95      cgg aag ccc ttt ggt gac ttt atg gag cct aag ttt gag ttt gct gtg      1461
96      Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val
97      355                      360                      365                      370
98      aag ttc aat gca ctg gaa tta gat gac agt gac ttg gct ata ttt ata      1509
99      Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile
100     375                      380                      385
101     gct gtc att att ctc agt gga gac cgc cca ggc ttg ctg aac gtg aag      1557
102     Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys
103     390                      395                      400
104     ccc atc gag gac atc caa gac aac ctg ctg cag gcc ctg gaa ctg cag      1605
105     Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln
106     405                      410                      415
107     ctc aag ctg aat cac cca gag tcc tct cag ctg ttc gcc aag gtg ctc      1653
108     Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Val Leu
109     420                      425                      430
110     cag aag atg aca gac ctc agg cag atc gtc aca gag cac gtg cag cta      1701
111     Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu
112     435                      440                      445                      450
113     ctg cat gtg atc aag aag aca gag aca gac atg agc ctt cac ccc ctg      1749
114     Leu His Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu
115     455                      460                      465
116     ctc cag gag atc tac aag gac ttg tat tagcaggaaa gtcccacccg      1796
117     Leu Gln Glu Ile Tyr Lys Asp Leu Tyr
118     470                      475
119     ctgacaacgt gttccttcta ttgattgcac tattatttttg agggaaaaaaa atctgacacc      1856
120     taagaaatttt actgtgaaaa agcatttaaa aacaaaaaagt tttagaacat gatctatttt      1916
121     atgcatatttg tttataaaga tacatttaca atttactttt aatattaaaa attaccacat      1976
122     tataaaaaaaaa aaaaaaaaaa aggaattcc      2005
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126 <213> ORGANISM: Mus musculus
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131     20                      25                      30
132     Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Ala Pro His Tyr
133     35                      40                      45
134     Glu Asp Ile Pro Phe Thr Arg Ala Asp Pro Met Val Ala Asp Tyr Lys
135     50                      55                      60
136     Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro
137     65                      70                      75                      80
138     Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Arg Pro
139     85                      90                      95
140     His Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys
141     100                     105                     110
142     Gly Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly
143     115                     120                     125
144     Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp

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145          130          135          140
146    Arg Cys Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys
147    145          150          155          160
148    Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn
149          165          170          175
150    Ala Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu
151          180          185          190
152    Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp
153          195          200          205
154    Leu Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe
155          210          215          220
156    Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr
157    225          230          235          240
158    Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly
159          245          250          255
160    Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser
161          260          265          270
162    Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val
163          275          280          285
164    Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Asn Ile Pro Gly Phe
165          290          295          300
166    Ile Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val
167    305          310          315          320
168    His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly
169          325          330          335
170    Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys
171          340          345          350
172    Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe
173          355          360          365
174    Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile
175          370          375          380
176    Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn
177    385          390          395          400
178    Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu
179          405          410          415
180    Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys
181          420          425          430
182    Val Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val
183          435          440          445
184    Gln Leu Leu His Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His
185          450          455          460
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188 <210> SEQ ID NO 3
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191 <213> ORGANISM: Saccharomyces cerevisiae
192 <220> FEATURE:
193 <221> NAME/KEY: CDS
194 <222> LOCATION: (35)...(544)

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199 gaa caa gca tgc gat att tgc cga ctt aaa aag ctc aag tgc tcc aaa 103
200 Glu Gln Ala Cys Asp Ile Cys Arg Leu Lys Lys Leu Lys Cys Ser Lys
201 10 15 20
202 gaa aaa ccg aag tgc gcc aag tgt ctg aag aac aac tgg gag tgt cgc 151
203 Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys Asn Asn Trp Glu Cys Arg
204 25 30 35
205 tac tct ccc aaa acc aaa agg tct ccg ctg act agg gca cat ctg aca 199
206 Tyr Ser Pro Lys Thr Lys Arg Ser Pro Leu Thr Arg Ala His Leu Thr
207 40 45 50 55
208 gaa gtg gaa tca agg cta gaa aga ctg gaa cag cta ttt cta ctg att 247
209 Glu Val Glu Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe Leu Leu Ile
210 60 65 70
211 ttt cct cga gaa gac ctt gac atg att ttg aaa atg gat tct tta cag 295
212 Phe Pro Arg Glu Asp Leu Asp Met Ile Leu Lys Met Asp Ser Leu Gln
213 75 80 85
214 gat ata aaa gca ttg tta aca gga tta ttt gta caa gat aat gtg aat 343
215 Asp Ile Lys Ala Leu Leu Thr Gly Leu Phe Val Gln Asp Asn Val Asn
216 90 95 100
217 aaa gat gcc gtc aca gat aga ttg gct tca gtg gag act gat atg cct 391
218 Lys Asp Ala Val Thr Asp Arg Leu Ala Ser Val Glu Thr Asp Met Pro
219 105 110 115
220 cta aca ttg aga cag cat aga ata agt gcg aca tca tca tcg gaa gag 439
221 Leu Thr Leu Arg Gln His Arg Ile Ser Ala Thr Ser Ser Ser Glu Glu
222 120 125 130 135
223 agt agt aac aaa ggt caa aga cag ttg act gta tcg ccg gaa ttc ccg 487
224 Ser Ser Asn Lys Gly Gln Arg Gln Leu Thr Val Ser Pro Glu Phe Pro
225 140 145 150
226 ggg atc cgt cga cgg tac cag ata tca gga tcc tgg cca gct agc tag 535
W--> 227 Gly Ile Arg Arg Arg Tyr Gln Ile Ser Gly Ser Trp Pro Ala Ser
228 155 160 165
229 gta gct aga gg 546
230 Val Ala Arg
231 <210> SEQ ID NO 4
232 <211> LENGTH: 169
233 <212> TYPE: PRT
234 <213> ORGANISM: Saccharomyces cerevisiae
235 <400> SEQUENCE: 4
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238 Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
239 20 25 30
240 Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
241 35 40 45
242 Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
243 50 55 60
244 Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile

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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text

227 W Line data has been corrected

Gly Ile Arg Arg Arg Tyr Gln Ile Ser Gly S

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CORRECTION SUMMARY
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Line Original Text

Corrected Data

227 Gly Ile Arg Arg Arg Tyr Gln Ile Ser Gly S Gly Ile Arg Arg Arg Tyr Gln Ile Ser Gly S

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PREVIOUSLY ERRORED SEQUENCES-EDITED

1 <210> 7
2 <211> 17
3 <212> DNA
4 <213> Saccharomyces cerevisiae
5 <400> 7
6 cggaggactg tcctccg

17